

INHERITANCE OF RESISTANCE TO COMMON BACTERIAL BLIGHT IN TEPARY BEANS

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Common bacterial blight (CBB) in common beans (*Phaseolus vulgaris* L.), incited by the bacterium *Xanthomonas campestris* pv. *phaseoli* (Smith) Dye (*Xcp*), is a serious disease affecting bean production. Resistant (R) common bean cultivars and lines have been released (Coyne and Schuster, Hort. Sci. 18:30-36, 1983; Michaels, Ann. Rep. Bean Imp. Coop. 35:40-41, 1992; and Park and Dhanvantari, Can. J. Pl. Sci. 67:685-695, 1987). However, higher levels of R to *Xcp* are needed in *P. vulgaris*. Sources of high R to *Xcp* have been reported in tepary bean (*Phaseolus acutifolius* A. Gray) (Honma, J. Hered. 47:217-220, 1956; McElroy, PhD thesis, Cornell Univ., NY, 1985). Honma (1956) reported a quantitative inheritance pattern for the reaction to *Xcp* in F_2 families in a *P. vulgaris* x *P. acutifolius* cross and McElroy (1985) in tepary crosses. Drijfhout and Blok (Euphytica 36:803-808, 1987) and Freytag (Ann. Rep. Bean Imp. Coop. 30:57, 1989) reported that R to *Xcp* in tepary beans was determined by one major dominant gene. The objective of the research reported here was to determine the inheritance of the reaction to different strains of *Xcp* in crosses between susceptible (S) and R tepary germplasm.

Germplasm and crosses: The following crosses were made among R x S and R and R tepary lines (NE) to *Xcp*; Nebr. #8-A(mod. R) (P_1) x Nebr. #8-B(R) (P_2), Nebr. #4-B(S) (P_3) x Nebr. #19(R) (P_4), Nebr. #4-B(S) (P_3) x CIAT-64005(R) (P_5), Nebr. #8-A(MR) (P_1) x Nebr. #4-B(S) (P_3), Nebr. #8-B(R) (P_2) x Nebr. #19(R) (P_4), and Nebr. #19(R) (P_4) x CIAT640005(R) (P_5).

Plants of the parents, F_2 , and F_3 populations of each cross were arranged separately on greenhouse benches, Lincoln, NE, in a RCBD using two replications. The approximate greenhouse day/night temperatures were $27 \pm 2^\circ\text{C} / 20 \pm 2^\circ\text{C}$ for F_2 populations and $28 \pm 3^\circ\text{C} / 21 \pm 3^\circ\text{C}$ for F_3 populations, respectively. The natural day lengths were approximately 13/11 and 14/10 (day/night) for F_2 and F_3 experiments, respectively.

Xcp strains V₃S₈ (A)(DR), LB-2 (B)(NE), and SC-4A (C)(NE) (all from A. Vidaver, UNL) were used. Leaflets of the first fully expanded trifoliolate leaf (with strains EK-11 and LB-2) and the second fully expanded trifoliolate leaf (with strain SC-4A) of each plant were inoculated using the multiple needle method. The percentage of the inoculated leaf area with CBB symptoms (necrosis, water-soaking and chlorosis) was recorded for each plant 21 days after inoculation.

High levels of R to *Xcp* were expressed by P_4 and P_5 (0% leaf area with symptoms). A moderate level of R was expressed by P_1 (0% to 30% leaf area with symptoms). P_3 was classified as S (11% to >30 leaf area with symptoms). Bimodal distributions for symptom classes were observed in the F_2 generations of the crosses P_3 x P_4 and P_3 x P_5 . Bimodality was not observed in the F_2 P_1 x P_3 . A good fit to a 3 : 1

ratio of R to S plants to the 3 *Xcp* strains was observed in the F_2 $P_3 \times P_4$, F_2 $P_3 \times P_5$, and F_2 $P_1 \times P_3$. It was hypothesized that there was a predominant effect of a single major gene affecting resistance to these 3 strains of *Xcp* in these crosses. The above hypothesis was confirmed in the F_3 generation of the crosses $P_3 \times P_5$ (inoculated with 3 strains) and $P_1 \times P_3$ (inoculated with strains LB-2 and SC-4A) based on satisfactory fits to 1:2:1 ratios of families nonsegregating for R, segregating for R and S, and nonsegregating for S. In the F_3 $P_1 \times P_3$, it was not possible to separate the F_3 families segregating for R and S and non segregating for S. However, it was possible to separate those nonsegregating for R for the above 2 classes using a chi-square contingency test. The number of F_3 families in the former two classes were then combined and compared with the number of F_3 families nonsegregating for R. A good fit to a 3 : 1 ratio of the former combined group to the latter resistant group confirmed the hypothesis based on the F_2 segregation. Transgressive segregation for increased S to the 3 strains was observed in the F_2 $P_1 \times P_2$ and was confirmed in the F_3 generation. This indicated that these parents differed in the genes controlling the different levels of R to the *Xcp* strains. No segregation for reactions to each of the 3 *Xcp* strains was observed in crosses of the R parents $P_2 \times P_4$ and $P_4 \times P_5$ indicating that these parents possessed the same dominant genes for R.

Recombinations of R and S plants to each of the *Xcp* strains were observed in the F_2 generations of the crosses $P_3 \times P_4$, $P_3 \times P_5$, and $P_1 \times P_3$. Coupling linkage was detected between the genes controlling the reactions to each of the 3 *Xcp* strains except that no linkage was observed between genes controlling the reactions to strains EK-11 and LB-2, and EK-11 and SC-4A in the cross $P_1 \times P_3$. This is the first report of different genes controlling the reaction to different *Xcp* strains and of their linkage relationships in the tepary crosses.

It would be useful to 'tag' these different dominant genes for R to different *Xcp* strains with molecular markers and to use these markers to pyramid these different genes into the *S. P. vulgaris*. It would be important to determine if the monogenic R observed in tepary is also expressed in a *P. vulgaris* background and if the levels of R to *Xcp* are maintained in *P. vulgaris* \times *P. acutifolius* lines derived from embryo rescue and congruity backcrossing following interspecific hybridization as described by Haghighi, K. R. and P. D. Ascher (Sex Plant Reprod. 1:51-58, 1988).